WHAT IS CLAIMED:

1. A method of determining whether a candidate compound modulates gene expression, comprising:

(a) providing a compound and a reporter gene in a system, wherein said reporter gene linked to an untranslated region comprising SEQ ID NO: 1; and

(b) detecting expression of said reporter gene in said system, wherein expression of said reporter gene is altered relative to expression of a reporter gene not linked to an untranslated region comprising SEQ ID NO: 1.

2. The method according to claim 1, wherein said untranslated region comprising SEQ ID NO: 1 is downstream of said reporter gene.

3. The method according to claim 2, wherein said untranslated region comprising SEQ ID NO: 1 is between about 1000 to about 500 residues upstream from the 5' end of a mRNA poly(A) tail.

4. The method according to claim 2, wherein said untranslated region comprising SEQ ID NO: 1 is between about 500 to about 100 residues upstream from the 5' end of a mRNA poly(A) tail.

5. The method according to claim 2, wherein said untranslated region comprising SEQ ID NO: 1 is between about 100 to about 60 residues upstream from the 5' end of a mRNA poly(A) tail.

6. The method according to claim 2, wherein said untranslated region comprising SEQ ID NO: 1 is about 80 residues upstream from the 5' end of a mRNA poly(A) tail.

7. The method according to claim 1, wherein an upstream open reading frame (uORF) is upstream of said reporter gene.

8. The method according to claim 1, wherein said reporter gene not linked to an untranslated region comprising SEQ ID NO: 1 is a reporter gene linked to an untranslated region from a control gene.

9. The method according to claim 1, wherein said expression of said reporter gene not linked to an untranslated region comprising SEQ ID NO: 1 is greater than zero.

10. The method according to claim 1, wherein said expression of said reporter gene not linked to an untranslated region comprising SEQ ID NO: 1 is greater than said expression of said reporter gene linked to an untranslated region comprising SEQ ID NO: 1.

11. The method according to claim 1, wherein said expression of said reporter gene not linked to an untranslated region comprising SEQ ID NO: 1 is less than said expression of said reporter gene linked to an untranslated region comprising SEQ ID NO: 1.

12. The method according to claim 1, wherein said reporter gene is located within a cell.

13. The method according to claim 12, wherein said cell is a mammalian cell.

14. The method according to claim 13, wherein said mammalian cell is a mammalian cancer cell.

15. The method according to claim 14, wherein said mammalian cancer cell is a MCF-7 cell.

16. The method according to claim 14, wherein said mammalian cancer cell is a Her2 overexpressing mammalian breast cancer cell.

17. The method according to claim 16, wherein said Her2 overexpressing mammalian breast cancer cell is a BT474 cell.

18. The method according to claim 1, wherein said reporter gene is translated *in vitro*.

19. The method according to claim 18, wherein said reporter gene is translated in the presence of a cellular extract.

20. The method according to claim 1, wherein said compound is a small-interfering RNA molecule.

21. A method of determining whether a candidate compound modulates gene expression, comprising:

(a) providing a reporter gene linked to an untranslated region from a target gene and a compound, wherein said untranslated region from a target gene is linked to SEQ ID NO: 1;

(b) detecting expression of said linked reporter gene;

(c) providing a reporter gene not linked to an untranslated region comprising SEQ ID NO: 1 and a compound; and

(d) detecting expression of said not linked reporter gene.

22. The method according to claim 21, wherein said untranslated region comprising SEQ ID NO: 1 is downstream of said reporter gene.

23. The method according to claim 21, wherein an uORF is upstream of said reporter gene.

24. The method according to claim 21, further comprising:

(e) comparing said expression of said linked reporter gene to said expression of said unlinked reporter gene.

25. A method comprising:

(a) providing a reporter gene linked to an untranslated region from a target gene and a compound, wherein said untranslated region from a target gene is linked to SEQ ID NO: 1; and

(b) detecting expression of said reporter gene, wherein said expression of said reporter gene is greater relative to expression of a reporter gene not linked to SEQ ID NO: 1.

26. The method according to claim 25, further comprising:

(c) detecting expression of said reporter gene not linked to SEQ ID NO: 1.

27. The method according to claim 25, further comprising:

(d) comparing said expression of said linked reporter gene to said expression of said not linked reporter gene.

28. A cell line comprising a reporter gene linked to an untranslated region comprising SEQ ID NO: 1.

29. The cell line according to claim 28, wherein said reporter gene is expressed at a level within an order of magnitude relative to a cell line comprising a reporter gene not linked to said untranslated region comprising SEQ ID NO: 1.

30. The cell line according to claim 28, wherein said reporter gene is stably expressed for six months or more.

31. The cell line according to claim 30, wherein said cell line is derived from a MCF-7 cell line.

32. A hybrid comprising a nucleic acid molecule comprising SEQ ID NO: 1 and a compound, wherein said compound is capable of inhibiting expression of a reporter gene linked to said nucleic acid molecule comprising SEQ ID NO: 1 relative to expression of a reporter gene not linked to a nucleic acid molecule comprising SEQ ID NO: 1.

33. The hybrid of claim 32, wherein the EC_{50} value of said compound is 5-20 fold less for expression of a reporter gene linked to an untranslated region comprising SEQ ID NO: 1 than for expression of a reporter gene not linked to an untranslated region comprising SEQ ID NO: 1.

34. The hybrid of claim 32, wherein the specificity of said compound is greater for a nucleic acid molecule comprising SEQ ID NO: 1 than for a nucleic acid molecule not comprising SEQ ID NO: 1.

35. The hybrid of claim 32, wherein the selectivity of said compound is at least ten-fold greater for a nucleic acid molecule comprising SEQ ID NO: 1 than for a nucleic acid molecule not comprising SEQ ID NO: 1.

36. The hybrid of claim 32, wherein said compound does not inhibit the activity of a protein encoded for by said reporter gene linked to said nucleic acid molecule comprising SEQ ID NO: 1

37. The hybrid of claim 32, wherein said nucleic acid molecule comprising SEQ ID NO: 1 is a RNA molecule.

38. The hybrid of claim 32, wherein said compound inhibits expression of said reporter gene linked to said nucleic acid molecule comprising SEQ ID NO: 1 in a Her2 overexpressing breast cancer cell more than it inhibits expression of said reporter gene linked to an untranslated region comprising SEQ ID NO: 1 in a MCF-7 cell.

39. The hybrid of claim 38, wherein said Her2 overexpressing breast cancer cell is a BT474 cell.

40. The hybrid of claim 32, wherein said compound is a nucleic acid molecule.

41. The hybrid of claim 32, wherein said compound is a quinazoline or quinoline or a derivative thereof either.

42. The hybrid of claim 32, wherein said compound is an inidazolopyridine or a derivative thereof.

43. The hybrid of claim 32, wherein said compound is an indazole or a derivative thereof.

44. A hybrid of a compound and a nucleic acid molecule comprising SEQ ID NO: 1, wherein said compound is capable of preferentially binding said nucleic acid molecule relative to a nucleic acid molecule not comprising SEQ ID NO: 1.

45. A substantially purified nucleic acid molecule comprising between 95% and 99% sequence identity with a nucleic acid molecule of SEQ ID NO: 1, a fragment thereof, or a complement of either.

46. The substantially purified nucleic acid molecule according to claim 45 that modulates expression of a gene selected from the group consisting of Mdm-2, Ship-2, Estrogen-

receptor-α, S-AdoMet, CCAAT/Enhancer-binding protein-α, and CCAAT/Enhancer-binding protein-β.

47. A substantially purified nucleic acid molecule consisting of SEQ ID NO: 1, a fragment thereof, or a complement of either.

48. The substantially purified nucleic acid molecule according to claim 47 that modulates expression of a gene selected from the group consisting of Mdm-2, Ship-2, Estrogen-receptor-α, S-AdoMet, CCAAT/Enhancer-binding protein-α, and CCAAT/Enhancer-binding protein-β.

49. A method for identifying a compound that modulates reporter gene expression comprising:

(a) providing a reporter gene linked to an untranslated region comprising SEQ ID NO: 1 and a cellular extract; and

(b) detecting expression of said reporter gene, wherein said compound modulates expression of said reporter gene relative to expression of a reporter gene not linked to an untranslated region comprising SEQ ID NO: 1.

50. The method of claim 49, wherein said cellular extract is from a cancer cell.

51. The method of claim 50, wherein said cancer cell is a Her2 overexpressing cancer cell.

52. The method of claim 51, wherein said Her2 overexpressing cancer cell is a BT474 cell.

53. A substantially purified polypeptide characterized by:

(a) a molecular weight of approximately 48-kDa on a 10-14% gradient SDS-polyacrylamide gel electrophoresis (SDS-PAGE);

(b) its ability to specifically bind SEQ ID NO: 1;

(c) its ability to suppresses uORF-dependent repression of gene expression; and

(d) its ability to cross-link to a Her2 3' UTR under physiological conditions.

54. The substantially purified polypeptide of claim 53, wherein said polypepide expression is regulated by a kinase.